SEQUENCE LISTING

#11/18

<110> Ashkenazi, Avi J.
 Baker, Kevin
 Gurney, Austin
 Wood, William

<120> Apo-2DcR

<130> 11669.29US02

<140> US 08/878,168

<141> 1997-06-18

<160> 17

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 259

<212> PRT

<213> HUMAN

<400> 1

Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arq Gln Glu 25 Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn 75 Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln Cys Lys 100 105 Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys Arg Lys Cys 120 Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp 135 140 Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu 150 155 Thr Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala 165 170 Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro 180 185 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala 200 205 Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala

Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr 225 230 235 240 Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Ile 245 250 255 Val Phe Val	爱 ····································
<210> 2 <211> 1180 <212> DNA <213> HUMAN	
<220> <221> CDS <222> (193)(969) <400> 2	
gctgtgggaa cctctccacg cgcacgaact cagccaacga tttctgatag atttttggga gtttgaccag agatgcaagg ggtgaaggag cgcttcctac cgttagggaa ctctggggac agagcgccc ggccgcctga tggccgaggc agggtgcgac ccaggaccca ggacggcgtc gggaaccata cc atg gcc cgg atc ccc aag acc cta aag ttc gtc gtc gtc Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val 1	120 180 231
atc gtc gcg gtc ctg ctg cca gtc cta gct tac tct gcc acc act gcc Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala 15 20 25	279
cgg cag gag gaa gtt ccc cag cag aca gtg gcc cca cag caa cag agg Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg 30 35 40 45	327
cac agc ttc aag ggg gag gag tgt cca gca gga tct cat aga tca gaa His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu 50 55 60	3,75
cat act gga gcc tgt aac ccg tgc aca gag ggt gtg gat tac acc aac His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn 65 70 75	423
gct tcc aac aat gaa cct tct tgc ttc cca tgt aca gtt tgt aaa tca Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser 80 85 90	471
gat caa aaa cat aaa agt tcc tgc acc atg acc aga gac aca gtg tgt Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys 95 100 105	519
cag tgt aaa gaa ggc acc ttc cgg aat gaa aac tcc cca gag atg tgc Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys 110 125	567

•	cgg Arg	aag Lys	tgt Cys	agc Ser	agg Arg 130	tgc Cys	cct Pro	agt Ser	Gly	gaa Glu 135	gtc Val	caa Gln	gtc Val	agt Ser	aat Asn 140	tgt Cys	615
	acg Thr	tcc Ser	tgg Trp	gat Asp 145	gat Asp	atc Ile	cag Gln	tgt Cys	gtt Val 150	gaa Glu	gaa Glu	ttt Phe	ggt Gly	gcc Ala 155	aat Asn	gcc Ala	663
	act Thr	gtg Val	gaa Glu 160	acc Thr	cca Pro	gct Ala	gct Ala	gaa Glu 165	gag Glu	aca Thr	atg Met	aac Asn	acc Thr 170	agc Ser	ccg Pro	gly ggg	711
	act Thr	cct Pro 175	gcc Ala	cca Pro	gct Ala	gct Ala	gaa Glu 180	gag Glu	aca Thr	atg Met	aac Asn	acc Thr 185	agc Ser	cca Pro	ggg Gly	act Thr	759
	cct Pro 190	gcc Ala	cca Pro	gct Ala	gct Ala	gaa Glu 195	gag Glu	aca Thr	atg Met	acc Thr	acc Thr 200	agc Ser	ccg Pro	Gly aaa	act Thr	cct Pro 205	807
	gcc Ala	cca Pro	gct Ala	gct Ala	gaa Glu 210	gag Glu	aca Thr	atg Met	acc Thr	acc Thr 215	agc Ser	ccg Pro	Gly	act Thr	cct Pro 220	gcc Ala	855
	cca Pro	gct Ala	gct Ala	gaa Glu 225	gag Glu	aca Thr	atg Met	acc Thr	acc Thr 230	agc Ser	ccg Pro	gly ggg	act Thr	cct Pro 235	gcc Ala	tct Ser	903
	tct Ser	cat His	tac Tyr 240	ctc Leu	tca Ser	tgc Cys	acc Thr	atc Ile 245	gta Val	gly ggg	atc Ile	ata Ile	gtt Val 250	cta Leu	att Ile	gtg Val	951
			att Ile				tgaa	agad	ctt o	cacto	gtgga	aa ga	aatt	cctt	=		999
	ccct	gcct	cc c	ctctc	gctgt	g tt	CCC	acaga	a cag	gaaac	gcc	tgcc	ccctc	gee d	ccaaa	ctctg aaaaaa aaaaaa	1059 1119 1179 1180
		_		~													

<210> 3

<211> 299

<212> PRT

<213> HUMAN

<400> 3

Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp 1 5 5 10 10 15 15 Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr 20 25 30 Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu 35 40 45

```
Lys Phe Val Val Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr
Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
Pro Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly
Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
            100
                                 105
                                                     110
Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys
        115
                                                 125
Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr
                                             140
Arg Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
                                         155
Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val
                165
                                     170
Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu
                                 185
Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met
                            200
                                                 205
Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn
                        215
                                             220
Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
                    230
                                         235
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser
                245
                                     250
Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro
            260
                                 265
Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
                            280
                                                 285
Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
                        295
      <210> 4
      <211> 1180
      <212> DNA
      <213> HUMAN
      <220>
      <221> CDS
      <222> (73)...(969)
      <221> sig_peptide
      \langle 222 \rangle (73)...(194)
      <400> 4
gctgtgggaa cctctccacg cgcacgaact cagccaacga tttctgatag atttttggga
                                                                        60
gtttgaccag ag atg caa ggg gtg aag gag cgc ttc cta ccg tta ggg aac
                                                                       111
              Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn
              -40
                                   -35
tct ggg gac aga gcg ccc cgg ccg cct gat ggc cga ggc agg gtg cga
                                                                       159
Ser Gly Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg
```

25,	The Facility of	-20	1 =
20,00		-20	-15
A	- 1		,

ccc Pro	ågg Arg -10	acc Thr	cag Gln	gac Asp	ggđ Gly	gtc Val -5	ggg Gly	aac Asn	cat His	acc Thr	atg Met 1	gcc Ala	cgg Arg	atc Ile	ccc Pro 5	207
aag Lys	acc Thr	cta Leu	aag Lys	ttc Phe 10	gtc Val	gtc Val	gtc Val	atc Ile	gtc Val 15	gcg Ala	gtc Val	ctg Leu	ctg Leu	cca Pro 20	gtc Val	255
cta Leu	gct Ala	tac Tyr	tct Ser 25	gcc Ala	acc Thr	act Thr	gcc Ala	cgg Arg 30	cag Gln	gag Glu	gaa Glu	gtt Val	ccc Pro 35	cag Gln	cag Gln	303
aca Thr	gtg Val	gcc Ala 40	cca Pro	cag Gln	caa Gln	cag Gln	agg Arg 45	cac His	agc Ser	ttc Phe	aag Lys	ggg Gly 50	gag Glu	gag Glu	tgt Cys	351
cca Pro	gca Ala 55	gga Gly	tct Ser	cat His	aga Arg	tca Ser 60	gaa Glu	cat His	act Thr	gga Gly	gcc Ala 65	tgt Cys	aac Asn	ccg Pro	tgc Cys	399
aca Thr 70	gag Glu	ggt Gly	gtg Val	gat Asp	tac Tyr 75	acc Thr	aac Asn	gct Ala	tcc Ser	aac Asn 80	aat Asn	gaa Glu	cct Pro	tct Ser	tgc Cys 85	447
ttc Phe	cca Pro	tgt Cys	aca Thr	gtt Val 90	tgt Cys	aaa Lys	tca Ser	gat Asp	caa Gln 95	aaa Lys	cat His	aaa Lys	agt Ser	tcc Ser 100	tgc Cys	495
acc Thr	atg Met	acc Thr	aga Arg 105	gac Asp	aca Thr	gtg Val	tgt Cys	cag Gln 110	tgt Cys	aaa Lys	gaa Glu	ggc Gly	acc Thr 115	ttc Phe	cgg Arg	543
aat Asn	gaa Glu	aac Asn 120	tcc Ser	cca Pro	gag Glu	atg Met	tgc Cys 125	cgg Arg	aag Lys	tgt Cys	agc Ser	agg Arg 130	tgc Cys	cct Pro	agt Ser	591
GJÀ aaa	gaa Glu 135	gtc Val	caa Gln	gtc Val	agt Ser	aat Asn 140	tgt Cys	acg Thr	tcc Ser	tgg Trp	gat Asp 145	gat Asp	atc Ile	cag Gln	tgt Cys	639
gtt Val 150	gaa Glu	gaa Glu	ttt Phe	ggt Gly	gcc Ala 155	aat Asn	gcc Ala	act Thr	gtg Val	gaa Glu 160	acc Thr	cca Pro	gct Ala	gct Ala	gaa Glu 165	687
gag Glu	aca Thr	atg Met	aac Asn	acc Thr 170	agc Ser	ccg Pro	ggg Gly	act Thr	cct Pro 175	gcc Ala	cca Pro	gct Ala	gct Ala	gaa Glu 180	gag Glu	735
aca Thr	atg Met	aac Asn	acc Thr 185	agc Ser	cca Pro	gly ggg	act Thr	cct Pro 190	gcc Ala	cca Pro	gct Ala	gct Ala	gaa Glu 195	gag Glu	aca Thr	783

•	• ,		•			÷										
atg Met	acc Thr	acc Thr 200	agc Ser	ccg Pro	gly aaa	act Thr	cct Pro 205	gcc Ala	cca Pro	gct Ala	gct Ala	gaa Glu 210	gag Glu	aca Thr	atg Met	8
acc Thr	acc Thr 215	agc Ser	ccg Pro	gly aga	act Thr	cct Pro 220	gcc Ala	cca Pro	gct Ala	gct Ala	gaa Glu 225	gag Glu	aca Thr	atg Met	acc Thr	8
acc Thr 230	agc Ser	ccg Pro	ggg	act Thr	cct Pro 235	gcc Ala	tct Ser	tct Ser	cat His	tac Tyr 240	ctc Leu	tca Ser	tgc Cys	acc Thr	atc Ile 245	9
gta Val	gly	atc Ile	ata Ile	gtt Val 250	cta Leu	att Ile	gtg Val	ctt Leu	ctg Leu 255	att Ile	gtg Val	ttt Phe	gtt Val			9
cag	aaac aaaa <: <: <:	gcc (aaa a 210> 211> 212>	tgcco aaaaa 5	cctg aaaa	CC C	caaaa	aaaaa	a aaa	aaaa	aaaa	aaaa	aaaa	aaa a	aaaa	cacaga aaaaaa	10 11 11
tgt	aaaa <: <: <:	210> 211> 212>	6 41		ta aa	ataga	acct	g caa	attai	taa	tct					
cag		400> cag (gacca	ac ct	cgcad	cacct	c gca	aaato	ccat	t					
	< : < :	210> 211> 212> 213>	49	AN												
Cys		400> Glu			Ser	Gly	Ser	Phe		Ala	Ser	Glu	Asn		Leu	
Arg	His	Cys		5 Ser	Cys	Ser	Lys		10 Arg	Lys	Glu	Met		15 Gln	Val	
Glu	Ile	Ser 35	20 Ser	Cys	Thr	Val	Asp 40	25 Arg	Asp	Thr	Val	Cys 45	30 Gly	Cys	Arg	
Lvs																

	<2 <2	210> 211> 212> 213>	48 PRT	AN												
Cvs		100> Pro		Thr	Glu	Glv	Val	Asp	Tvr	Thr	Agn	Δla	Ser	Asn	Δen	
1				5				_	10					15		
GIU	Pro	Ser	Cys 20	Pne	Pro	Cys	Thr	Va⊥ 25	Cys	Lys	Ser	Asp	GIn 30	Lys	His	
Lys	Ser	Ser 35	Cys	Thr	Met	Thr	Arg 40	Asp	Thr	Val	Cys	Gln 45	Cys	Lys	Glu	
	<2 <2	210> 211> 212> 213>	70 D NA	ΛN												
				aggaa	ag tt	gggd	cctca	a tgg	gacaa	atga	gata	aaagg	gtg (gctaa	aagctg	60 70
	<2 <2	210> 211> 212> 213>	1799 DNA													
	<2	220> 221> 222>))	. (135	72)										•
aata	acgco	cga c	gcat gate	gcccg	ga to c ato	ctact g gaa	ttaa a caa	a ggg	gctga g gga	aaac a cag	ccad g aad	gggg	cat g	gagag g gco	ccacaa gactat gct a Ala	60 120 172
tcg Ser	ggg Gly	gcc Ala	cgg Arg 15	aaa Lys	agg Arg	cac His	ggc Gly	cca Pro 20	gga Gly	ccc Pro	agg Arg	gag Glu	gcg Ala 25	cgg Arg	gga Gly	220
gcc Ala	agg Arg	cct Pro 30	Gly aaa	ctc Leu	cgg Arg	gtc Val	ccc Pro 35	aag Lys	acc Thr	ctt Leu	gtg Val	ctc Leu 40	gtt Val	gtc Val	gcc Ala	268
														caa Gln		316
gac Asp 60	cta Leu	gct Ala	ccc Pro	cag Gln	cag Gln 65	aga Arg	gcg Ala	gcc Ala	cca Pro	caa Gln 70	caa Gln	aag Lys	agg Arg	tcc Ser	agc Ser 75	364

ccc Pro	tca Ser	gag Glu	gga Gly	ttg Leu 80	tgt Cys	cca Pro	cct Pro	gga Gly	cac His 85	cat His	atc Ile	tca Ser	gaa Glu	gac Asp 90	ggt Gly	412
aga Arg	gat Asp	tgc Cys	atc Ile 95	tcc Ser	tgc Cys	aaa Lys	tat Tyr	gga Gly 100	cag Gln	gac Asp	tat Tyr	agc Ser	act Thr 105	cac His	tgg Trp	460
aat Asn	gac Asp	ctc Leu 110	ctt Leu	ttc Phe	tgc Cys	ttg Leu	cgc Arg 115	tgc Cys	acc Thr	agg Arg	tgt Cys	gat Asp 120	tca Ser	ggt Gly	gaa Glu	508
gtg Val	gag Glu 125	cta Leu	agt Ser	ccc Pro	tgc Cys	acc Thr 130	acg Thr	acc Thr	aga Arg	aac Asn	aca Thr 135	gtg Val	tgt Cys	cag Gln	tgc Cys	556
gaa Glu 140	gaa Glu	ggc Gly	acc Thr	ttc Phe	cgg Arg 145	gaa Glu	gaa Glu	gat Asp	tct Ser	cct Pro 150	gag Glu	atg Met	tgc Cys	cgg Arg	aag Lys 155	604
tgc Cys	cgc Arg	aca Thr	Gly ggg	tgt Cys 160	ccc Pro	aga Arg	gly ggg	atg Met	gtc Val 165	aag Lys	gtc Val	ggt Gly	gat Asp	tgt Cys 170	aca Thr	652
								cac His 180								700
gga Gly	gtc Val	aca Thr 190	gtt Val	gca Ala	gcc Ala	gta Val	gtc Val 195	ttg Leu	att Ile	gtg Val	gct Ala	gtg Val 200	ttt Phe	gtt Val	tgc Cys	748
								ctt Leu								796
tca Ser 220	ggt Gly	ggt Gly	ggt Gly	Gly aaa	gac Asp 225	cct Pro	gag Glu	cgt Arg	gtg Val	gac Asp 230	aga Arg	agc Ser	tca Ser	caa Gln	cga Arg 235	844
cct Pro	Gly	gct Ala	gag Glu	gac Asp 240	aat Asn	gtc Val	ctc Leu	aat Asn	gag Glu 245	atc Ile	gtg Val	agt Ser	atc Ile	ttg Leu 250	cag Gln	892
ccc Pro	acc Thr	cag Gln	gtc Val 255	cct Pro	gag Glu	cag Gln	gaa Glu	atg Met 260	gaa Glu	gtc Val	cag Gln	gag Glu	cca Pro 265	gca Ala	gag Glu	940
								ccc Pro								988

gaa Glu	ccg Pro 285	gca Ala	gaa Glu	gct Ala	gaa Glu	agg Arg 290	tct Ser	cag Gln	agg Arg	agg Arg	agg Arg 295	ctg Leu	ctg Leu	gtt Val	cca Pro	1036
gca Ala 300	aat Asn	gaa Glu	ggt Gly	gat Asp	ccc Pro 305	act Thr	gag Glu	act Thr	ctg Leu	aga Arg 310	cag Gln	tgc Cys	ttc Phe	gat Asp	gac Asp 315	1084
ttt Phe	gca Ala	gac Asp	ttg Leu	gtg Val 320	ccc Pro	ttt Phe	gac Asp	tcc Ser	tgg Trp 325	gag Glu	ccg Pro	ctc Leu	atg Met	agg Arg 330	aag Lys	1132
ttg Leu	ggc Gly	ctc Leu	atg Met 335	gac Asp	aat Asn	gag Glu	ata Ile	aag Lys 340	gtg Val	gct Ala	aaa Lys	gct Ala	gag Glu 345	gca Ala	gcg Ala	1180
ggc Gly	cac His	agg Arg 350	gac Asp	acc Thr	ttg Leu	tac Tyr	acg Thr 355	atg Met	ctg Leu	ata Ile	aag Lys	tgg Trp 360	gtc Val	aac Asn	aaa Lys	1228
acc Thr	ggg Gly 365	cga Arg	gat Asp	gcc Ala	tct Ser	gtc Val 370	cac His	acc Thr	ctg Leu	ctg Leu	gat Asp 375	gcc Ala	ttg Leu	gag Glu	acg Thr	1276
ctg Leu 380	gga Gly	gag Glu	aga Arg	ctt Leu	gcc Ala 385	aag Lys	cag Gln	aag Lys	att Ile	gag Glu 390	gac Asp	cac His	ttg Leu	ttg Leu	agc Ser 395	1324
tct Ser	gga Gly	aag Lys	ttc Phe	atg Met 400	tat Tyr	cta Leu	gaa Glu	ggt Gly	aat Asn 405	gca Ala	gac Asp	tct Ser	gcc Ala	wtg Xaa 410	tcc Ser	1372
aaad ggca ccgt	aacto etcto attat ettgt eaato	gga o ccc a ttt t cgc o gta a	eteca ateca etata gtaet aatgo	agtca aacat aagct ttga cttta	ag ta c ac cg aa ag at at tt	aggaa cccag atgtg ttgg tattt	aagto gtgga gataa gttto cattt	g cca a tgg a taa g gga c ggg	acaat gaaca aggad atgto gctad	tgt atcc cact catt catt	tgta atgg gttt gtaa	atgad aactt gaaat ctcad agatd	ccg g tt d tgt d cag d cca t	gtact cacto ctgga cactt	aaaaag ggaag gcactt atcatt tttta caaaaa ggccgc	1432 1492 1552 1612 1672 1732 1792

<210> 11

<211> 411

<212> PRT

<213> HUMAN

<400> 11

Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln 55 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe 105 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro 120 Cys Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe 135 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys 150 155 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile 165 170 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala 185 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp 200 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly 215 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp 230 235 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro 250 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn 265 270 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala 280 285 Glu Arg Ser Gln Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp 295 300 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val 310 315 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp 330 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr 345 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala 355 360 365 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu 375 Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met 390 395 Tyr Leu Glu Gly Asn Ala Asp Ser Ala Xaa Ser 405

<210> 12

<211> 29

<212> DNA

<213> HUMAN

<400> 12

Ile Leu Val Val Thr Leu Val Val Pro Leu Leu Val Ala Val Leu

Ile Val Cys Cys Cys Ile Gly Ser Gly Cys Gly Gly Asp Pro Lys Cys

Met Asp Arg Val Cys Phe Trp Arg Leu Gly Leu Leu Arg Gly Pro Gly

Ala Glu Asp Asn Ala His Asn Glu Ile Leu Ser Asn Ala Asp Ser Leu

Ser Thr Phe Val Ser Glu Gln Gln Met Glu Ser Gln Glu Pro Ala Asp
260 265 270

Leu Thr Gly Val Thr Val Gln Ser Pro Gly Glu Ala Gln Cys Leu Leu
275 280 285

Gly Pro Ala Glu Ala Glu Gly Ser Gln Arg Arg Leu Leu Val Pro

215

230

29

30

11

250

235

```
295
                                             300
Ala Asn Gly Ala Asp Pro Thr Glu Thr Leu Met Leu Phe Phe Asp Lys
                    310
                                         315
Phe Ala Asn Ile Val Pro Phe Asp Ser Trp Asp Gln Leu Met Arg Gln
                325
                                     330
Leu Asp Leu Thr Lys Asn Glu Ile Asp Val Val Arg Ala Gly Thr Ala
                                 345
Gly Pro Gly Asp Ala Leu Tyr Ala Met Leu Met Lys Trp Val Asn Lys
        355
                            360
                                                 365
Thr Gly Arg Asn Ala Ser Ile His Thr Leu Leu Asp Ala Leu Glu Arg
                        375
Met Glu Glu Arg His Ala Lys Glu Lys Ile Gln Asp Leu Leu Val Asp
                    390
                                         395
Ser Gly Lys Phe Ile Tyr Leu Glu Asp Gly Thr Gly Ser Ala Val Ser
                405
Leu Glu
      <210> 15
      <211> 74
      <212> PRT
```

<400> 15

<213> HUMAN

 Val
 Met
 Asp
 Ala
 Val
 Pro
 Ala
 Arg
 Arg
 Trp
 Lys
 Glu
 Phe
 Val
 Arg
 Thr

 Leu
 Gly
 Leu
 Arg
 Glu
 Ala
 Glu
 Ile
 Glu
 Ala
 Val
 Glu
 Val
 Glu
 Ile
 Gly
 Ile
 I

<210> 16 <211> 78 <212> PRT

<213> HUMAN

<210> 17

<211> 77 <212> PRT <213> HUMAN